

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 11, 2005, 11:53:58 ; Search time 66 Seconds  
(without alignments)  
169.108 Million cell updates/sec

Title: US-09-824-134-2\_COPY\_130\_245  
Perfect score: 593  
Sequence: 1 FEAGAAAGAAPEEDLCAAF.....QEVQQAQDLQNRSGAMSPMS 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID      | Description        |
|------------|-------|-------------|--------|---------|--------------------|
| 1          | 593   | 100.0       | 208    | A56912  | FADD protein - hum |
| 2          | 115.5 | 19.5        | 656    | I49299  | receptor interacti |
| 3          | 114.5 | 19.3        | 1856   | B35049  | ankyrin 1, erythro |
| 4          | 114.5 | 19.3        | 1880   | A35049  | ankyrin 1, erythro |
| 5          | 114.5 | 19.3        | 1881   | SJHUK   | ankyrin 1, erythro |
| 6          | 112.5 | 19.0        | 1848   | S37771  | ankyrin, erythrocy |
| 7          | 112.5 | 19.0        | 1862   | I49502  | ankyrin - mouse    |
| 8          | 111.5 | 18.8        | 671    | T09479  | serine/threonine p |
| 9          | 103   | 17.4        | 2039   | T15347  | ankyrin-related un |
| 10         | 96.5  | 16.3        | 3924   | S37431  | ankyrin 2, neuro   |
| 11         | 93    | 15.7        | 324    | JC2395  | Fas antigen precu  |
| 12         | 86    | 14.5        | 1765   | T42714  | ankyrin 3, splice  |
| 13         | 86    | 14.5        | 1940   | T42715  | ankyrin 3, splice  |
| 14         | 86    | 14.5        | 1943   | T42713  | ankyrin 3, splice  |
| 15         | 86    | 14.5        | 1957   | A45627  | myosin heavy chain |
| 16         | 86    | 14.5        | 1961   | T42716  | ankyrin 3, splice  |
| 17         | 86    | 14.5        | 4377   | A55575  | ankyrin 3, long sp |
| 18         | 84    | 14.2        | 1138   | S37773  | ankyrin, erythrocy |
| 19         | 84    | 14.2        | 1955   | T30934  | myosin-like protei |
| 20         | 83    | 14.0        | 657    | A53545  | protein p84 - huma |
| 21         | 81    | 13.7        | 312    | A56911  | TRADD protein - hu |
| 22         | 79.5  | 13.4        | 724    | A38749  | 3-phosphatidylinos |
| 23         | 76.5  | 12.9        | 374    | H75002  | methyl-accepting c |
| 24         | 75.5  | 12.7        | 549    | B86264  | hypothetical prote |
| 25         | 75    | 12.6        | 313    | MXRBR   | nonstructural prot |
| 26         | 74.5  | 12.6        | 455    | GQHUT1  | tumor necrosis fac |
| 27         | 74    | 12.5        | 427    | 1 GQHUN | nerve growth facto |
| 28         | 74    | 12.5        | 433    | A32992  | cyclin B1 - human  |
| 29         | 73.5  | 12.4        | 2325   | T15566  | hypothetical prote |

ALIGNMENTS

RESULT 1

A56912  
FADD protein - human  
N:Alternate names: FAS-associating death domain containing protein FADD; mediator of re  
C:Species: Homo sapiens (man)  
C>Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: A56912; I38041  
R:Chinnaiyan, A.M.; O'Rourke, K.; Tewari, M.; Dixit, V.M.  
Cell 81, 505-512, 1995  
A>Title: FADD, a novel death domain-containing protein, interacts with the death domain  
A:Reference number: A56912; MUID:95277837; PMID:7538907  
A:Accession: A56912  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-208 <CHI>  
A:Cross-references: UNIPROT:Q13158; GB:U24231; NID:G809486; PIDN:AAA86517.1; PID:G80948  
R:Bollin, M.P.; Vafiolomeev, E.E.; Pancer, Z.; Matt, I.L.; Camonis, J.H.; Wallach, D.  
J. Biol. Chem. 270, 7795-7798, 1995  
A>Title: A novel protein that interacts with the death domain of Fas/APO1 contains a se  
A:Reference number: I38041; MUID:95229578; PMID:7536190  
A:Accession: I38041  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-31,'V',33-208 <RES>  
A:Cross-references: EMBL:X84709; NID:G791037; PIDN:CAAS9197.1; PID:G791038  
C:Genetics:  
A:Gene: GDB:FADD; MORT1  
A:Cross-references: GDB:I320394  
C:Superfamily: receptor-induced toxicity mediator MORT1  
C:Keywords: apoptosis

Query Match 100.0%; Score 593; DB 2; Length 208;

Best Local Similarity 100.0%; Pred. No. 5.3e-49; Mismatches 0; Indels 0; Gaps 0;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSPTKIDSIEDRYPRNTERV 60

Db 82 FEAGAAAGAAPEEDLCAAFNVICNVGKDWRLARQLKVSPTKIDSIEDRYPRNTERV 141

QY 61 RESLRWKTKENATVAHLVGLRSCQNVLVADLVQEVQQAQDLQNRSGAMSPMS 116

Db 142 RESLRWKTKENATVAHLVGLRSCQNVLVADLVQEVQQAQDLQNRSGAMSPMS 197

RESULT 2

I49299

receptor interacting protein RIP - mouse

C:Species: Mus musculus (house mouse)

C>Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 09-Jul-2004

C:Accession: I49299

R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.

Cell 81, 513-523, 1995

A:Title: RIP: a novel protein containing a death domain that interacts with Fas/APO-1 (c  
A:Reference number: A56913; MUID:95277838; PMID:7538908

A:Accession: I49299  
A>Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-656 <RES>  
A:Cross-references: UNIPROT:Q60855; EMBL:U25995; NID:G829618; PIDN:AAB60487.1; PID:G8296  
C:Genetics: RIP  
A:Gene: RIP  
F:15-293/Domain: protein kinase homology <KIN>

Query Match 19.5%; Score 115.5; DB 2; Length 656;  
Best Local Similarity 34.9%; Pred. No. 0.0039;  
Matches 29; Conservative 22; Mismatches 29; Indels 3; Gaps 3;

QY 21 NVICDNVGVKWRRLARQLKVSVDTKIDSIEDRYPRN-ITERVRESLRWKTE-KENATVA 78  
DB 573 NPINELGRQWKNCAKLGFTSQIDYERDGLKVKYQMLQKWLREGTKGATVG 632

QY 79 HLVGAL-RSCOMNLVADLVQEVQ 100  
DB 633 KLAQALHQCCRIDLNLHIRASQ 655

RESULT 3  
B35049  
ankyrin 1, erythrocyte splice form 3 - human  
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N:Contains: ankyrin 2.2, erythrocyte  
C:Species: Homo sapiens (man)  
C:Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 10-Jul-1998  
C:Accession: B35049  
R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K  
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990  
A:Title: cDNA sequence for human erythrocyte ankyrin.  
A:Reference number: A35049; MUID:90175370; PMID:1689849  
A:Accession: B35049  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1856 <LAM>  
C:Genetics:  
A:Gene: GDB:ANK1; ANK  
A:Cross-references: GDB:118737; OMIM:182900  
A:Map position: 8p11.2-8p11.2  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing  
F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>  
F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>  
F:44-76/Domain: ankyrin repeat homology <AN01>  
F:77-109/Domain: ankyrin repeat homology <AN02>  
F:110-142/Domain: ankyrin repeat homology <AN03>  
F:143-171/Domain: ankyrin repeat homology <AN04>  
F:172-204/Domain: ankyrin repeat homology <AN05>  
F:205-237/Domain: ankyrin repeat homology <AN06>  
F:238-270/Domain: ankyrin repeat homology <AN07>  
F:271-303/Domain: ankyrin repeat homology <AN08>  
F:304-336/Domain: ankyrin repeat homology <AN09>  
F:337-369/Domain: ankyrin repeat homology <AN10>  
F:370-402/Domain: ankyrin repeat homology <AN11>  
F:403-435/Domain: ankyrin repeat homology <AN12>  
F:436-468/Domain: ankyrin repeat homology <AN13>  
F:469-501/Domain: ankyrin repeat homology <AN14>  
F:502-534/Domain: ankyrin repeat homology <AN15>  
F:535-567/Domain: ankyrin repeat homology <AN16>  
F:568-600/Domain: ankyrin repeat homology <AN17>  
F:601-633/Domain: ankyrin repeat homology <AN18>  
F:634-666/Domain: ankyrin repeat homology <AN19>  
F:667-699/Domain: ankyrin repeat homology <AN20>  
F:700-732/Domain: ankyrin repeat homology <AN21>  
F:733-765/Domain: ankyrin repeat homology <AN22>  
F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 19.3%; Score 114.5; DB 2; Length 1856;

Best Local Similarity 28.1%; Pred. No. 0.016;  
Matches 32; Conservative 26; Mismatches 49; Indels 7; Gaps 2;

QY 8 GAAPGEEDLCAPNVICDNVGVKWRRLARQLKVSVDTKIDSIEDRYPRNLTFRVRESLRW 67  
DB 1395 GSLSGTEQAEQMAVISEHLGSLWAEARELOFQSVEDINRIRVENPNLSLEQSVALLNLW 1454

QY 68 KNTKENATVAHLVGALRSCOMNLVADLVQ-EVQQARDLQ-----NRSGAMSP 114  
DB 1455 VIREGQNANMENLYTALQSIDRGEIVNMLEGSRQSRNLKPDRTDRTDYSLSP 1508

RESULT 4  
A35049  
ankyrin 1, erythrocyte splice form 2 - human  
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N:Contains: ankyrin 2.2, erythrocyte  
C:Species: Homo sapiens (man)  
C:Date: 27-Jul-1990 #sequence\_revision 01-Oct-1992 #text\_change 09-Jul-2004  
C:Accession: A35049  
R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K  
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990  
A:Title: cDNA sequence for human erythrocyte ankyrin.  
A:Reference number: A35049; MUID:90175370; PMID:1689849  
A:Accession: A35049  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1880 <LAM>  
A:Cross-references: UNIPROT:P16157; GB:M28880  
C:Genetics:  
A:Gene: GDB:ANK1; ANK  
A:Cross-references: GDB:118737; OMIM:182900  
A:Map position: 8p11.2-8p11.2  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing; cytoskeleton  
F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>  
F:2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>  
F:44-76/Domain: ankyrin repeat homology <AN01>  
F:77-109/Domain: ankyrin repeat homology <AN02>  
F:110-142/Domain: ankyrin repeat homology <AN03>  
F:143-171/Domain: ankyrin repeat homology <AN04>  
F:172-204/Domain: ankyrin repeat homology <AN05>  
F:205-237/Domain: ankyrin repeat homology <AN06>  
F:238-270/Domain: ankyrin repeat homology <AN07>  
F:271-303/Domain: ankyrin repeat homology <AN08>  
F:304-336/Domain: ankyrin repeat homology <AN09>  
F:337-369/Domain: ankyrin repeat homology <AN10>  
F:370-402/Domain: ankyrin repeat homology <AN11>  
F:403-435/Domain: ankyrin repeat homology <AN12>  
F:436-468/Domain: ankyrin repeat homology <AN13>  
F:469-501/Domain: ankyrin repeat homology <AN14>  
F:502-534/Domain: ankyrin repeat homology <AN15>  
F:535-567/Domain: ankyrin repeat homology <AN16>  
F:568-600/Domain: ankyrin repeat homology <AN17>  
F:601-633/Domain: ankyrin repeat homology <AN18>  
F:634-666/Domain: ankyrin repeat homology <AN19>  
F:667-699/Domain: ankyrin repeat homology <AN20>  
F:700-732/Domain: ankyrin repeat homology <AN21>  
F:733-765/Domain: ankyrin repeat homology <AN22>  
F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 19.3%; Score 114.5; DB 2; Length 1880;  
Best Local Similarity 28.1%; Pred. No. 0.016;  
Matches 32; Conservative 26; Mismatches 49; Indels 7; Gaps 2;

QY 8 GAAPGEEDLCAPNVICDNVGVKWRRLARQLKVSVDTKIDSIEDRYPRNLTFRVRESLRW 67  
DB 1395 GSLSGTEQAEQMAVISEHLGSLWAEARELOFQSVEDINRIRVENPNLSLEQSVALLNLW 1454

QY 68 KNTKENATVAHLVGALRSCOMNLVADLVQ-EVQQARDLQ-----NRSGAMSP 114  
DB 1455 VIREGQNANMENLYTALQSIDRGEIVNMLEGSRQSRNLKPDRTDRTDYSLSP 1508

RESULT 5  
SJHUK

ankyrin 1, erythrocyte splice form 1 - human  
N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N;Contains: ankyrin 2.2  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text\_change 09-Jul-2004  
C;Accession: S08275; A33219; PC2220; A35443  
R;Lux, S.E.; John, K.M.; Bennett, V.  
Nature 344, 36-42, 1990  
A;Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure  
A;Reference number: S08275; MUID:90158830; PMID:2137557  
A;Accession: S08275  
A;Molecule type: mRNA  
A;Residues: 1-1881 <LU1>  
A;Cross-references: UNIPROT:P16157; EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702  
A;Accession: A33219  
A;Molecule type: protein  
A;Residues: 2-7,'X',9-17,'X',19-20,'T',22-30;733-749,'A',751-753;828-833,'X',835-855,'X',  
X',1367;1383-1427;1601-1630;1686-1698,'D',1700;1763-1772 <LUX>  
A;Note: 845-Arg and 1392-Thr were also found  
R;Hermann, J.; Barel, M.; Prade, R.  
Biochem. Biophys. Res. Commun. 204, 453-460, 1994  
A;Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane  
A;Reference number: PC2220; MUID:95071348; PMID:7526850  
A;Accession: PC2220  
A;Molecule type: protein  
A;Residues: 910-929 <HER>  
R;Davis, L.H.; Bennett, V.  
J. Biol. Chem. 265, 10589-10596, 1990  
A;Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger  
A;Reference number: A35443; MUID:90285190; PMID:2141335  
A;Accession: A35443  
A;Molecule type: protein  
A;Residues: 'X',5,'X',7-12;403-417,'X',419-422,'H',424,'LQ';797-800,'L',802-814;862-863,  
C;Genetics:  
A;Gene: GDB:ANK1; ANK  
A;Cross-references: GDB:I18737; OMIM:182900  
A;Map position: 8p11.2-8p11.2  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing; phosphoprotein  
F;2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>  
F;2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <DOM1>  
F;2-827/Region: anion exchange predicted protein binding  
F;44-76/Domain: ankyrin repeat homology <AN01>  
F;77-109/Domain: ankyrin repeat homology <AN02>  
F;110-142/Domain: ankyrin repeat homology <AN03>  
F;143-171/Domain: ankyrin repeat homology <AN04>  
F;172-204/Domain: ankyrin repeat homology <AN05>  
F;205-237/Domain: ankyrin repeat homology <AN06>  
F;238-270/Domain: ankyrin repeat homology <AN07>  
F;271-303/Domain: ankyrin repeat homology <AN08>  
F;304-336/Domain: ankyrin repeat homology <AN09>  
F;337-369/Domain: ankyrin repeat homology <AN10>  
F;370-402/Domain: ankyrin repeat homology <AN11>  
F;403-435/Domain: ankyrin repeat homology <AN12>  
F;436-468/Domain: ankyrin repeat homology <AN13>  
F;469-501/Domain: ankyrin repeat homology <AN14>  
F;502-534/Domain: ankyrin repeat homology <AN15>  
F;535-567/Domain: ankyrin repeat homology <AN16>  
F;568-600/Domain: ankyrin repeat homology <AN17>  
F;601-633/Domain: ankyrin repeat homology <AN18>  
F;634-666/Domain: ankyrin repeat homology <AN19>  
F;667-699/Domain: ankyrin repeat homology <AN20>  
F;700-732/Domain: ankyrin repeat homology <AN21>  
F;733-765/Domain: ankyrin repeat homology <AN22>  
F;766-798/Domain: ankyrin repeat homology <AN23>  
F;788-1382/Domain: 62K #status predicted <DOM2>  
F;1383-1881/Region: spectrin binding  
F;182-1382/Region: 55K #status predicted <DOM3>

R;White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.  
Mamm. Genome 3, 281-285, 1992  
A;Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory domain  
A;Reference number: 149502; MUID:92345717; PMID:1386265  
A;Accession: I49502  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1862 <RES>  
A;Cross-references: UNIPROT:Q02357; GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940  
C;Genetics:  
A;Gene: Ank-1  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing  
F;40-72/Domain: ankyrin repeat homology <AN01>  
F;73-105/Domain: ankyrin repeat homology <AN02>  
F;106-138/Domain: ankyrin repeat homology <AN03>  
F;139-167/Domain: ankyrin repeat homology <AN04>  
F;168-200/Domain: ankyrin repeat homology <AN05>  
F;201-233/Domain: ankyrin repeat homology <AN06>  
F;234-266/Domain: ankyrin repeat homology <AN07>  
F;267-299/Domain: ankyrin repeat homology <AN08>  
F;300-332/Domain: ankyrin repeat homology <AN09>  
F;333-365/Domain: ankyrin repeat homology <AN10>  
F;366-398/Domain: ankyrin repeat homology <AN11>  
F;399-431/Domain: ankyrin repeat homology <AN12>  
F;432-464/Domain: ankyrin repeat homology <AN13>  
F;465-497/Domain: ankyrin repeat homology <AN14>  
F;498-530/Domain: ankyrin repeat homology <AN15>  
F;531-563/Domain: ankyrin repeat homology <AN16>  
F;564-596/Domain: ankyrin repeat homology <AN17>  
F;597-629/Domain: ankyrin repeat homology <AN18>  
F;630-662/Domain: ankyrin repeat homology <AN19>  
F;663-695/Domain: ankyrin repeat homology <AN20>  
F;696-728/Domain: ankyrin repeat homology <AN21>  
F;729-761/Domain: ankyrin repeat homology <AN22>  
F;762-794/Domain: ankyrin repeat homology <AN23>  
Query Match 19.08; Score 112.5; DB 2; Length 1862;  
Best Local Similarity 29.08; Pred. No. 0.024;  
Matches 29; Conservative 27; Mismatches 37; Indels 7; Gaps 2;  
QY 22 VICNVGKWRRLARQLKVSQTKIDSDIEDYPRNLTFRVRSRIWKNTKKNATVAHLV 81  
DB 1405 VIREHLGLSMAELARELQFVSVDINIRVENPNSLDQSTALLTLWVDREGENAKMENLY 1464  
QY 82 GALRSCQNLVADLVO-EVQARDLQ-----NRSGAMSP 114  
DB 1465 TALNRIDRSEIVNLEGGQSRNLKPRRHGRDREYSLSP 1504  
RESULT 8  
T09479  
serine/threonine protein kinase (EC 2.7.1.1-) RIP - human  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
A;Accession: T09479; I38992  
R;Huang, J.; Heu, H.B.; Baichwal, V.R.; Goeddel, D.V.  
submitted to the EMBL Data Library, August 1998  
A;Reference number: Z16685  
A;Accession: T09479  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-671 <HUA>  
A;Cross-references: UNIPROT:Q13546; EMBL:U50062; NID:g3426026; PID:g3426027  
R;Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.  
Cell 81, 513-523, 1995  
A;Title: RIP: A novel protein containing a death domain that interacts with Fas/APO-1 (CD95)  
A;Reference number: A56913; MUID:95277838; PMID:7538908  
A;Accession: I38992  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 300-513 <RES>  
A;Cross-references: EMBL:U25994; NID:g829616; PIDN:AAC50137.1; PID:g829617

C;Genetics:  
A;Gene: RIP  
C;Keywords: ATP binding; phosphotransferase  
Query Match 18.8%; Score 111.5; DB 2; Length 671;  
Best Local Similarity 36.4%; Pred. No. 0.0096;  
Matches 28; Conservative 19; Mismatches 27; Indels 3; Gaps 3;  
QY 23 ICNVGKWRRLARQLKVSQTKIDSDIEDYPRNLTFRVRSRIWKNTKKNATVAHL 80  
DB 590 IRENLGKHWKNCARKLGFTQSQIDEIDHDYERDGLKEKVYQMLQKWYMRGKIGATVGL 649  
QY 81 VGALRSC-OMNLVADLIV 96  
DB 650 AQALHQCSDRIDLUSSLI 666  
RESULT 9  
T15347  
ankyrin-related unc-44 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
A;Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282  
R;Gattung, S.  
submitted to the EMBL Data Library, February 1996  
A;Description: The sequence of C. elegans cosmid B0350.  
A;Reference number: Z18332  
A;Accession: T15347  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-2039 <GAT>  
A;Cross-references: UNIPROT:Q17489; EMBL:U50071; NID:g1208871; PID:g1208873; PIDN:AAA934  
A;Accession: T15346  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1000, 'SKLQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVA  
32, 'S', 2034-2035, 'GSPTRSVPEEHRHSQHDHGGST' <GA2>  
A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1  
A;Accession: T15344  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'QRSTIVAESTSEQVPE', 1934-1935, 'E  
<GA3>  
A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208874; PIDN:AAA93444.1  
A;Accession: T15345  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVPE  
PTRSVPEEHRHSQHDHGGST' <GA4>  
R;Otsuka, A.J.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontrakulpoo  
J. Cell Biol. 129, 1081-1092, 1995  
A;Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Cae  
A;Reference number: A57282; MUID:95263663; PMID:7744957  
A;Accession: A57282  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-852, 'GGG', 856-1000, 'SKLQHRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWE  
, 'SHRED', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHS' <OTS>  
A;Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608  
A;Accession: B57282  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E  
V', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPTRSVPEEHRHS', 1984-1985, 'EDEHGS', 'E  
4, 'TIV', 1828, 'ESTS', 1833, 'OV', 1836, 'E', 1934-1935, 'EQS', 1939, 'ESES', 1944, 'REDDGTIVT', 194  
A;Cross-references: GB:U21733; NID:g790603; PIDN:AAA85853.1; PID:g790604  
C;Genetics:

A;Gene: CESP:unc-44  
A;Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979/2  
C;Superfamily: ankyrin; ankyrin repeat homology  
F;164-192/Domain: ankyrin repeat homology <AN04>  
F;358-390/Domain: ankyrin repeat homology <AN1>  
F;391-423/Domain: ankyrin repeat homology <AN11>  
Query Match 17.4%; Score 103; DB 2; Length 2039;  
Best Local Similarity 31.9%; Pred. No. 0.21; Mismatches 15; Gaps 3;  
Matches 30; Conservative 15; Indels 41; Gaps 8; Gaps 3;  
QY 23 ICDNVGKWRRLARLQKVSDDTKIDSDYPRNLTERVRESRIWKNTKENATVAHLVG 82  
Db 1504 VLKIGIGADWPRLEPRHDIHQIRQYNP---GQECKNTLKIWIHLKKEDANQDNLQ 1560  
QY 83 ALRSCQMLVADLQVEVQARD--LQNRSGMSP 114  
Db 1561 ALRQIGRD---DIVRSIAYGEPDALINYSQADSP 1591  
RESULT 10  
S37431  
ankyrin 2, neuronal long splice form - human  
N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid  
N;Contains: ankyrin 2, short form  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004  
C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569  
R;Chan, W.  
submitted to the EMBL Data Library, September 1993  
A;Reference number: S37431  
A;Accession: S37431  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-3924 <CHA>  
A;Cross-references: UNIPROT:Q01484; EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406287  
R;Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.  
J. Cell Biol. 114, 241-253, 1991  
A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a  
A;Reference number: A39643; MUID:91302466; PMID:1830053  
A;Accession: A39643  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2077 <OT1>  
A;Cross-references: GB:X56957  
A;Accession: B39643  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1443, 3585-3924 <OTT>  
A;Cross-references: EMBL:X56958  
R;Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,  
Genomics 10, 858-866, 1991  
A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.  
A;Reference number: A40334; MUID:92009921; PMID:1833308  
A;Accession: A40334  
A;Molecule type: DNA  
A;Residues: 463-474, PE', 477-495 <TSE>  
A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648  
R;Chan, W.; Kordeli, E.; Bennett, V.  
J. Cell Biol. 123, 1463-1473, 1993  
A;Title: 440-KD ankyrinB: structure of the major developmentally regulated domain and se  
A;Reference number: A49462; MUID:94075409; PMID:8253844  
A;Accession: A49462  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-3924 <RES>  
A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288  
C;Genetics:  
A;Gene: GDB:ANK2  
A;Cross-references: GDB:127607; OMIM:106410  
A;Map position: 4q25-4q27  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing

F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>  
F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>  
F;63-95/Domain: ankyrin repeat homology <AN01>  
F;96-128/Domain: ankyrin repeat homology <AN02>  
F;129-161/Domain: ankyrin repeat homology <AN03>  
F;162-190/Domain: ankyrin repeat homology <AN04>  
F;191-223/Domain: ankyrin repeat homology <AN05>  
F;232-264/Domain: ankyrin repeat homology <AN06>  
F;265-297/Domain: ankyrin repeat homology <AN07>  
F;298-330/Domain: ankyrin repeat homology <AN08>  
F;331-363/Domain: ankyrin repeat homology <AN09>  
F;364-396/Domain: ankyrin repeat homology <AN10>  
F;397-429/Domain: ankyrin repeat homology <AN11>  
F;430-462/Domain: ankyrin repeat homology <AN12>  
F;463-495/Domain: ankyrin repeat homology <AN13>  
F;496-528/Domain: ankyrin repeat homology <AN14>  
F;529-561/Domain: ankyrin repeat homology <AN15>  
F;562-594/Domain: ankyrin repeat homology <AN16>  
F;595-627/Domain: ankyrin repeat homology <AN17>  
F;628-660/Domain: ankyrin repeat homology <AN18>  
F;661-693/Domain: ankyrin repeat homology <AN19>  
F;694-726/Domain: ankyrin repeat homology <AN20>  
F;727-759/Domain: ankyrin repeat homology <AN21>  
F;760-792/Domain: ankyrin repeat homology <AN22>  
F;793-825/Domain: ankyrin repeat homology <AN23>  
Query Match 16.3%; Score 96.5; DB 2; Length 3924;  
Best Local Similarity 24.3%; Pred. No. 1.8; Mismatches 21; Indels 15; Gaps 1;  
Matches 25; Conservative 21; Mismatches 42; Indels 15; Gaps 1;  
QY 23 ICDNVGKWRRLARLQKVSDDTKIDSDYPRNLTERVRESRIWKNTKENATVAHLVG 82  
Db 3543 IADHLGFSWTELARELDFTTEQIHQIRIENPNLSQDSQYLLKIMLWDGKHATDTNLVE 3602  
QY 83 ALRSCQMLVADLQV-----EVQARDLQNRSG 110  
Db 3603 CLTKINRMDIVHLMETNPTEPQERISHSYAEIEQTITLDHSEG 3645  
RESULT 11  
JC2395  
Fas antigen precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text change 09-Jul-2004  
C;Accession: JC2395; PC2246  
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.  
Biochem. Biophys. Res. Commun. 198, 666-674, 1994  
A;Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liv  
A;Reference number: JC2395; MUID:94128114; PMID:7507668  
A;Accession: JC2395  
A;Molecule type: mRNA  
A;Residues: 1-324 <KIM>  
A;Cross-references: UNIPROT:Q63199; DBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d100  
A;Experimental source: thymus  
A;Accession: PC2246  
A;Molecule type: mRNA  
A;Residues: 1-62, 'RPT', <K12>  
A;Cross-references: DBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g46848  
A;Experimental source: liver  
C;Genetics:  
A;Introns: 62/1  
C;Superfamily: tumor necrosis factor receptor type 1 (TNPR1); NGF receptor repeat homol  
C;Keywords: transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-324/Product: Fas antigen #status predicted <MAT>  
F;44-79/Domain: NGF receptor repeat homology <NGF>  
F;81-124/Domain: NGF receptor repeat homology <NG4>  
F;171-188/Domain: transmembrane #status predicted <TMW>  
Query Match 15.7%; Score 93; DB 2; Length 324;  
Best Local Similarity 28.2%; Pred. No. 0.24; Mismatches 16; Indels 8; Gaps 2;  
Matches 22; Conservative 16; Mismatches 32; Indels 8; Gaps 2;

Qy 23 ICNVGVKWRRLARQLKVSDTKTIDSYPRNLTERVRESLRWKNTKEKNAIVHLVG 82  
Db 231 ICDA-----KKFARQHKIPESKIDTEIHNSPDAAEQIKQLLCWYQSHGKTGACQALI.Q 285  
Qy 83 ALRSCQNLVLADLVQEVQ 100  
Db 286 GLRKANR---CDIAERIQ 300

RESULT 12  
T42714  
ankyrin 3, splice form 2 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C:Accession: T42714  
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, I.  
J. Cell Biol. 130, 313-330, 1995  
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene  
the repeat domain.  
A:Reference number: Z22237; MUID:95340633; PMID:7615634  
A:Accession: T42714  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-1765 <PEP>  
A:A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:G710548; PID:G710551; PIDN:AAB01605  
A:Experimental source: strain C57BL/6J; kidney  
C:Genetics:  
A:Gene: Ank3  
A:Map position: 10  
A:Introns: 1587/1  
C:Superfamily: ankyrin; ankyrin repeat homology  
C:Keywords: alternative splicing

|    |   |        |                |        |              |      |
|----|---|--------|----------------|--------|--------------|------|
|    | Query Match   | 14.5%; | Score 86;      | DB 2;  | Length 1765; |      |
|    | Best Local Similarity   | 29.0%; | Pred. No. 7.4; |        |              |      |
|    | Matches   | 27;    | Conservative   | 18;    | Mismatches   | 44;  |
|    |   |        |                | Indels | 4;           | Gaps |
|    |   |        |                |        |              | 3;   |
| QY | 22 VICNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERTVRESLRITWKNTEKENATVAHLV  | 81     | :              | :      | :            | :    |
| Dd | 1494 IVADHGLGSMTELARELNFVSDEINQIRVENPNSLSIQSFMLKKKWTRDGNKNAITDAIT | 1543   | :              | :      | :            | :    |
| QY | 82 GALSRCQNVLVDLVQEVQ--QAARDLONRSGAMS                             | 113    | :              | :      | :            | :    |
| Dd | 1544 SVL--TKINRI-DIVTLLEGPIFYDGYNISGTARS                          | 1573   | :              | :      | :            | :    |

RESULT 13  
 T42715  
 ankrynin 3, splice form 3 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
 C:Accession: T42715  
 RJPeters, L.L.; John, K.M.; Lu, F.M.; Eichler, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.  
 J. Cell Biol. 130, 313-330, 1995  
 A:Title: Ank3 (epithelial ankrynin), a widely distributed new member of the ankrynin gene  
 the repeat domain.  
 A:Reference number: Z22237; MUID:95340633; PMID:7615634  
 A:Accession: T42715  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1940 <PET>  
 A:Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604  
 A:Experimental source: strain C57BL/6J; kidney  
 C:Genetics:  
 A:Gene: Ank3  
 A:Map position: 10  
 A:Introns: 834/1  
 C:Superfamily: ankrynin; ankrynin repeat homology  
 C:Keywords: alternative splicing  
  
 Query Match 14.5%; Score 86; DB 2; Length 1940;  
 Best Local Similarity 29.0%; Pred. No. 8.2;  
 Matches 27; Conservative 18; Mismatches 44; Indels 4; Gaps 3;

|    |      |  |                 |             |      |
|----|------|--|-----------------|-------------|------|
| Qy | 22   | VICDNVCKDWRRLARQLKVSDFTKIDSIDIEDYRPNRT | TERVRESLRITWONT | EKENATVAHLV | 81   |
| Db | 1463 | IVADHUGLSTWELARLNFSDVEINQIRVENPNSLISOF | MLLKWKVTRD      | KGNA        | 1522 |
| Qy | 82   | GALRSQMNVLADLVQEVQ-QARDLQNRSGAMS       | 113             |             |      |
| Db | 1523 | SVL--TKINRI-DIVTLLEGPIFDVGNISGTRS      | 1552            |             |      |

PRECIPIT. T. 14

ankyrin 3, splice form 1 - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
 C/Accession: T42713  
 R/Peters, L.D.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; T  
 J. Cell Biol. 130, 313-330, 1995  
 A/Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyr  
 the repeat domain.  
 A/Reference number: Z22237; MUID:95340633; PMID:7615634  
 A/Accession: T42713  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-1943 <PET>  
 A/Cross-references: UNIPROT:Q61307; EMBL:L40632; NID:G710548; PID:G710550; PIDN  
 A/Experimental source: strain C57BL/6J; kidney  
 C/Genetics:  
 A/Gene: Ank3  
 A/Map position: 10  
 A/Introns: 855/1  
 C/Function:  
 A/Description: supposed to play an important role in the polarized distribution  
 A/Note: major kidney ankyrin  
 C/Superfamily: ankyrin; ankyrin repeat homology  
 C/Keywords: alternative splicing

|                       |        |                  |                |              |
|-----------------------|--------|------------------|----------------|--------------|
| Query Match           | 14.5%; | Score 86;        | DB 2;          | Length 1943; |
| Best Local Similarity | 29.0%; | Pred. NO. 8.3;   |                |              |
| Matches               | 27;    | Conservative 18; | Mismatches 44; | Indels 4;    |
| Gaps                  | 3;     |                  |                |              |

  

|    |      |   |      |
|----|------|---|------|
| QY | 22   | VTCNVGKDWRLARQLKVKSTKIDSIEDRYPRNLTERVRESLRIRWKNTEKENATVAHLV | 81   |
|    | :    | :   | :    |
|    | :    | :   | :    |
|    | :    | :   | :    |
| Db | 1466 | IVADHLGLSWTELARELNFVSDEINQIRVENPNSLISQSFWLLKKWVTRDGNATTDALT | 1525 |
|    | :    | :   | :    |
|    | :    | :   | :    |
|    | :    | :   | :    |
| QY | 82   | GAIRSCQNNLVADLVQEVQ-QARDLQNRSGAMS                           | 113  |
|    | :    | :   | :    |
|    | :    | :   | :    |
|    | :    | :   | :    |
| Db | 1526 | SVL--TKINRI-DIVTLLEGFIYDGNISGTR                             | 1555 |
|    | :    | :   | :    |
|    | :    | :   | :    |
|    | :    | :   | :    |

DEC 11 1955

K56021 15  
 myosin heavy chain [similarity] - nematode (Brugia malayi)  
 C1Species: Brugia malayi  
 C1Date: 22-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C1Accession: A45627; B45526  
 R1Werner, C.; Rajan, T.V.  
 Mol. Biochem. Parasitol. 50, 261-268, 1992  
 A1Title: Characterization of a myosin heavy chain gene from Brugia malayi.  
 A1Reference number: A45627; MUID:92159006; PMID:1741013  
 A1Accession: A45627  
 A1Status: Preliminary  
 A1Molecule type: DNA  
 A1Residues: 1-1957 <WER>  
 A1Cross-references: UNIPROT.Q04009; GB:M74000; NID:G156086; PID:AAA73080.1; PID:AAA73080.2  
 A1Note: sequence extracted from NCBI backbone (NCBIN:83576, NCBIP:83578)  
 R1Werner, C.; Higashi, G.I.; Yates, J.A.; Rajan, T.V.  
 Mol. Biochem. Parasitol. 35, 209-218, 1989  
 A1Title: Differential recognition of two cloned Brugia malayi antigens by antibodies  
 A1Reference number: A45526; MUID:89314048; PMID:2664506  
 A1Accession: B45526  
 A1Status: preliminary  
 A1Molecule type: DNA

A:Residues: 'R',1491-1556 <WE2>  
A:Cross-references: GB:J04645  
A>Note: the authors translated the codon TTG for residue 1540 as Lys  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: ATP; nucleotide binding; P-loop  
F:89-773/Domain: myosin motor domain homology <MMOT>  
F:179-186/Region: nucleotide-binding motif A (P-loop)

Query Match 14.5%; Score 86; DB 2; Length 1957;  
Best Local Similarity 28.0%; Pred. No. 8.3; Mismatches 12; Gaps 4;  
Matches 26; Conservative 23; Indels 32; Indels 12; Gaps 4;

QY 25 DNVGKDWRLAROLKYSYDTKIDSIIE---DRYPNLTERTVRESLRIRWNTKENTATVAHLV 81  
DB 1053 NEIEKQKRGKIGGLKVAQENMEEIERQHEIESNLAKKGESEAQAITTRLEEQ----DLL 1108

QY 82 GALRSQ---MNLVADLVQEVQOARDLQNRSGA 111  
DB 1109 GSLKTCQRTTQNRRISELELENER--QSRKA 1139

Search completed: February 11, 2005, 16:41:35  
Job time : 67 secs

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